IFWO

RAW SEQUENCE LISTING   DATE: 08/23/2004
PATENT APPLICATION: US/10/676,873A   TIME: 11:15:35

Input Set : A:\COTH-P01-002.TXT
Output Set: N:\CRF4\08232004\J676873A.raw

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 4 <110> APPLICANT: Chan, John
 5         Baynes, Brian
 6         Zhang, Shengsheng
 8 <120> TITLE OF INVENTION: METHODS OF ENGINEERING SPATIALLY
 9         CONSERVED MOTIFS IN POLYPEPTIDES
12 <130> FILE REFERENCE: COTH-P01-002
14 <140> CURRENT APPLICATION NUMBER: US 10/676,873A
15 <141> CURRENT FILING DATE: 2003-09-30
17 <150> PRIOR APPLICATION NUMBER: US 60/414,688
18 <151> PRIOR FILING DATE: 2002-09-30
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 474
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Nucleotide sequence of TNF alpha chain b mutation
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33 <400> SEQUENCE: 1
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35 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120
36 gtggagctga gagataacca gctggtggtg ccatcagagg gcctgtacct catctactcc 180
37 caggtcctct tcaagggcca aggctgcccc tccacccatg tgctcctcac ccacaccatc 240
38 agccgcatcg ccgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300
39 tgccagaggg agaccccaga gggggctgag gccaagccct ggtatgagcc catcgatctg 360
40 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgac 420
41 tatctcgact ttgccgagtc tgggcaggtc tactttggga tcattgccct gtga      474
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44 <211> LENGTH: 157
45 <212> TYPE: PRT
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Protein sequence of TNF alpha chain b mutation
50         b_tyr_119_asp
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54 1               5                   10                  15
55 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
56             20                  25                  30
57 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
58             35                  40                  45
59 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
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60      50                    55                    60
61 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
62 65                    70                    75                    80
63 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
64                    85                    90                    95
65 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
66                    100                    105                    110
67 Pro Gln Tyr Glu Pro Ile Asp Leu Gly Gly Val Phe Gln Leu Glu Lys
68          115                    120                    125
69 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
70      130                    135                    140
71 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
72 145                    150                    155
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76 <211> LENGTH: 474
77 <212> TYPE: DNA
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: Nucleotide sequence of TNF alpha chain c mutations
82      c_tyr_119_his, c_tyr_59_ser
84 <400> SEQUENCE: 3
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86 caagctgagg ggcagctcca gtggctgaac cgccgggcca atgccctcct ggccaatggc 120
87 gtggagctga gagataacca gctggtggtg ccatcagagg gcctgtacct catcagttcc 180
88 caggtcctct tcaagggcca aggctgcccc tccacccatg tgctcctcac ccacaccatc 240
89 agccgcatcg ccgtctccta ccagaccaag gtcaacctcc tctctgccat caagagcccc 300
90 tgccagaggg agaccccaga gggggctgag gccaagccct ggtatgagcc catccatctg 360
91 ggaggggtct tccagctgga gaagggtgac cgactcagcg ctgagatcaa tcggcccgac 420
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96 <212> TYPE: PRT
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100 <223> OTHER INFORMATION: Protein sequence of TNF alpha chain c mutations
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103 <400> SEQUENCE: 4
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105  1                    5                    10                    15
106 Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
107                    20                    25                    30
108 Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
109          35                    40                    45
110 Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Ser Ser Gln Val Leu Phe
111      50                    55                    60
112 Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
113 65                    70                    75                    80
114 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
115                    85                    90                    95
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116 Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
117                 100                 105                 110
118 Pro Gln Tyr Glu Pro Ile His Leu Gly Gly Val Phe Gln Leu Glu Lys
119             115                 120                 125
120 Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Leu Phe
121         130                 135                 140
122 Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
123 145                 150                 155
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VERIFICATION SUMMARY   DATE: 08/23/2004
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